

FIGURE 1

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA
 GAGAAGCGCCTGCAGCCAACCAAGGTCAGGCTGTGCTCACAGTTCCTCTGGCGGCATGTAA
 AGGCTCCACAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC
 CAAGCCCTGGACCTGCCGAGCCTGGCACTGAGGCAGCGCTGACGCTACTGTGAGGGAAGA
 AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCT
 CTGTGGAGGCGAGGCCAGTGGAGCCCACTGAGGCAGGGCTGCTTGGCAGCCACCGGCTGCA
 ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATG
 TGAGGAGCCGCCCCGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
 ATAACCACCATTTTGCAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
 CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTTGAGGGCACTGAGGAGGCTC
 GCCAAGAGAGTTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCAGGACAAGTGCA
 CCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTCGCTCAACTCCAAGGAG
 CCTGAGGTGCTTCTGGAGAACCAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT
 GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG
 TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGAACATGAACTCGCGGGTCACGCAGCTG
 TACATGCAGCTCCTGCACGAGATCATCCGAAGCGGGACAACGCGTTGGAGCTCTCCAGCT
 GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
 TGGAGCACAAAGTACCAGCACCTGGCCACACTGGCCCCAACCAATCAGAGATCATCGCGCAG
 CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCAGCCACCCCCGCTGC
 CCGCCCCGGGTCTACCAACCAACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG
 AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCACTATGCCACTCTC
 ACCAGCTCCCATCTTCCACCGACAAGCCGTGCGGCCCATGGAGAGACTGCCTGCAGGCCCT
 GGAGGTGGCCACGACACCAAGCTCCATCTACCTGGTGAAGCCGGAGAACCAACCCGCTCA
 TGCAGGTGTGGTGGCACCAGAGACAGACCCCGGGGGCTGGACCGTCATCCAGAGACGCTG
 GATGGCTCTGTAACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA
 CGGCGAATAGTGGCTGGGCTGGGAGAACATTACTGGCTGACGAACCAAGGCAACTACAAAC
 TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAGTCTTTGCAGAAATACGCCAGTTTCCGC
 CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGCGGCGCTACCATGGCAATGCGGGTGA
 CTCTTTACATGGCACAACGGCAAGCAGTTCACCACCCCTGGACAGAGATCATGATGTCTACA
 CAGGAAACTGTGCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC
 CTCAACGGGGTCTGGTACGCGGGGGCCATTACGGAGCGCGTACCAGGACGGAGTCTACTG
 GGCTGAGTTCGAGGAGGGTCTTACTCACTCAAGAAAGTGGTATGATGATCCGACCGAACC
 CCAACACCTTCCACTAAGCCAGCTCCCCCTCTGACCTCTCTGGCCATTGGCAGGACGCCA
 CCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCTCACCAGTTCATCCTGAGGCTGGGA
 GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAACCTGAATCGAT
 ACGGTTTTTTCTGCTCTCTACTTTCTCTTACACCAGACAGCCCCATCATGTCTCCAGGACA
 GGACAGGACTACAGACAACCTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVTGAICVNSKEPEVLLNRRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRNMNSRVTLQLYMQLLHEIIRKRDNALELSQLENRILNQADMLQLASKYKDEHKYQHL
ATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSDTPSGPWRDCLQALDGHDTSSIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFRRNWETKYQGFGNIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKRLRLGRYHGNAGDSFTWHNGKQFTTLDRDHVYTGNCADHYQ
KGGWYWNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMIRPNPTFH
```

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479**Amidation site.**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
 GGAGTGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCCTAGAAGAGGGT
 GTTCCCTCTTTCCGGGGTCCCTCACCAGAAGAGGTTCTTGGGGTTCGCCCTTCTGAGGAGGGT
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATCC
 TCAACTCCAGTTATGAAAACAGTACTTGAAAACTGAAACTACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCCTGTTCCGGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTACGGTCACTCCAGTGGAAT
 GAAAAGTGTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAA
 TGATAAGATTTGATGTTTTTGTCTGCTGTCATCTACTTTGTCTGGAATGTCTAAATGTTTC
 TGTAGCAGAAAAACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ

AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNVDGLVLDTLAVIRTLVDK

Important features:**Signal peptide:**

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCCAGTGC GGAGAA
 GCCCCGGCAAACGCGAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGGCGGCGGGTATCGCCAGCTCGCTCATCCGTGAGAAGGGCAAGCCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGACACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTGTGAAAATATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
 GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAACAAACAGG
 CAGAGTTCATACTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTEPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 7

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAACCAGTCAACAAGAGTAAGACAACATAG

FIGURE 8

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
```

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRSSPSKNRGLCNGNLVDIFSKVIRIFGLKKRRRLR
RQDPQLKGI VTRLYCRQGYLLQMHDPDGLDGTDDSTNSTLFLNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLPSELFTECKFKESVFENYVYIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCA
 GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAACTCGAACCAGCT
 GTGTCCAGACTGAGGCCCATTTGCATTGTTTAAACATACTTAGAAAAATGAAGTGTTTCAATTTT
 TAACATTCTCTCCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGT
 GCTTGGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGCGCTCTCCCCGTGTCTCTCCA
 CGACTCGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCAGAGGAGGCCGA
 CGTGCCCGAGCTCCTCGGGGGTCCCGCCGCGAGCTTCTCTCGCCTTCGCATCTCCTCC
 TCGCGCGTCTTGGAC**ATG**CCAGGAATAAAAGGATACTCACTGTTACCATTCTGGCTCTCTG
 TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
 CAGGACAGTGTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCTGCCGAGGAGACATG
 ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCCCCGGACAACCCCTGTGTATCGAGG
 GCCCTACTCGAACCCTACTCGACCCCTACTCAGGTCGGTACCCAGCAGCTGCCCCACCAC
 TCTCAGCTCCAACTATCCCACGATCTCCAGGCTCTTATATGCCGCTTTGGATACCAGATG
 GATGAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAAGTCAACCC
 CACCCAGATCTGCATCAATACTGAAGCGGGTACACCTGCTCTGCACGACGAGTATTTGGC
 TTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGT
 GCGAATGTTCTTGATCTATTCTTTGATACATGCAACCTGGTTTTACCCTCAATGAGGATGG
 AAGGCTTTGCCAAGATGTGAACGAGTGTGCCACCCGAGAACCCTGCGTGCAAACTCGCTCA
 ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACCTTGAGGAAGATGGCGTT
 CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCTCTGCCAACATGAGTGTGTGAA
 CCAGCCCGGCACATACTTCTGCTCTGCCCTCCAGGCTACATCTGCTGGATGACAACCGAA
 GCTGCCAAGACATCAACGAATGTGAGCACAGGAACACACGCTGCAACCTGCAGCAGACGTGC
 TACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG
 GATCAGTGATAACCGCTGTATGTGTCCTGCTGAGAACCCTGGCTGCAGAGACCGCCTTTA
 CCATCTTGTACCGGGACATGGACGTGGTGTGAGGACGCTCCGTTCCCGCTGACATCTCCAA
 ATGCAAGCCACGACCCGCTACCCTGGGGCTATTACATTTTCCAGATCAAATCTGGGAATGA
 GGGCAGAGAATTTTACATGCCGCAACCGGGCCCATCAGTGCCACCCTGGTGTGACACGCC
 CCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAATGATCACTGTCAACATGTCAATC
 AACTTCAGAGGCAGCTCCGTGATCCGACTCGGATATATGTGTCGAGTACCCATT**CTG**AGC
 CTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTTGGCACCAAGGGACAGGAGAAGAGGAAA
 TAACAGAGAGAATGAGAGCGACACAGAGCTTAGGCATTTCTGCTGAACGTTTCCCCGAAGA
 GTCACCCCGGACTTCTGTACTCTCACCTGTACTATTGCAGACCTGTCACTCTGCAGACTTG
 CCACCCCGAGTTCCATGACACAGTTATCAAAAAGTATTATCATCTGCTCCCTGTAGTAGAAGA
 TTGTTGGTGAATTTTCAAGGCCCTTCAGTTTATTTCCACTATTTTCAAAGAAAATAGATTAGG
 TTTGGCGGGGCTGTAGTCTATGTTCAAAGACTGTGAACAGCTTGTGTCACTTCTTCACTCT
 TTCCACTCTCTCTCTCTGTGTTACTGCTTTGCAAAAGACCCGGAGCTGGCGGGGAACCTC
 GGGAGTAGCTAGTTGTCTTTTGCGTACACAGAGAAGGCTATGTAACAAACACACAGCAGGA
 TCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGCCTGGTATTTTCAACCAATAAAGAAG
 TTTCACTTGTCTTAAATTTGATATAACGGTTTAAATCTGTCTTGTCTATTGGATTTTTT
 AAAAAATATGTCTAGAAATCTCTCGAAAGGCCCTTCAGACACATGCTATGTTCTGTCTCTCC
 AAACCCAGTCTCTCTCCATTTAGCCCCAGTGTTTTCTTTGAGGACCCTTAATCTTGTCTTT
 CTTTAGAATTTTTACCCAATTGGATTGGAATGCAGAGGTCTCCAACTGATTAAATATTTGA
 AGAGA

MFGIKRILTVTILALCLSPGNAQAQCTNGFDLDRSGQCCLDIDECRTIPEACRGDMCMCVNQ
NGGYLCIPRTNPVYRGPSYNPYSTPYSGPYAAAPLSPAPNYPTISRPLICRFGYQMDENQ
CVDVDECATDSHCNPQTQICINTEGYTCSCTDGYWLLBGQCCLDIDECRYGYCQQLCANVPG
SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSLICRCDPGYELEEDGVHCSDM
DECSFSEFLCQHECVNQFGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQG
GFKCIDPIRCEKYLRIISDNRCMPAENPGCRDQPFITLYRDMDVVSGRSVPADIFQMQATT
RYPGAIYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPREIQLDLEMITVNTVINFRGS
SVIRLIYVSOYF

Signal peptide:

amino acids 1-25

amino acids 283-287, 296-300

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316

amino acids 144-156, 181-193, 262-274

amino acids 54-57

amino acids 131-166, 172-205, 211-245, 251-286

CAGGTCCAACATGCACCTCGGTTCTATCGATTGAATTCGCCGGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCAGCGCTCCGAACACAGGTCCTTGCTGTCGACGAGAGCACTGTTTGTGCTG
 GAAGGAGGAGTGGCGGGCTGCCCGGGCTCTCCCTGCGCCCTCTCTCAGTGGATGCTT
 CCAGGACACCTTGCTTGGGCGAGGGAGGGCACAGGCTGCACATCTCAAGTGGGGTGGGACCA
 GGGTCGCCCTGCCCCAGCATCAAGTCTCCCTTGGGCGCCGCTGGCCCTGCAGACTCTCA
 GGGCTAAGTCTCTGTGTGCTTTTGGTTGCCACTTAGAAGAGGCTCCGCTTGACTAAGAT
 AGCTTAGAAGGAGCACATGAGGAGGACTGCATCTGCTCTGGTGGGCGCTTCTCTTGGGCCCT
 GCTCAGGCTCGCCTGAGCCTGCGACTGTGGGGAAGAATATGGCTTCAGATCGCCGACTT
 TGCCTACCGGCACCTAGAATCCGTGCGCGCTGGCTTCCGGGCCAATGTGACTACACTGAGCC
 TGTCAAGCAACCGGCTGCGAGGCTTCCGCGAGGTGCTCTCAGGAGGCTGCCCTGCTGCAG
 TCGCTGTGGCTGGCGACACATGAGATGAGATCCGACAGCTGGCGCGAGGCTGGCCCTCTCTGAG
 CCATCTCAAGAGCTGGACCTGACCCACATCTCATCTCTGACTTTGCGCTGGAGGCACCTGC
 ACAACCTCAGCTGCCCTCCAATTGCTCAAGATGGACGCAACGAGCTGACCTTATCCCCGCG
 GAGCCTTCCGCGAGCTTCGTGCTCTGCGCTCGCTGCAACTAACCAACCGCTTGACAC
 ATTTGGCGAGGCGACCTTCAACCCTGCTACCCGCGCTGTCCCACTGCAGATCAACCGGAAC
 CTTTCGACTGCACTGGGCACTGTGTGGCTGACAGCATGGGCCCTGACCAACGGGCTGTC
 ATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGCTGAG
 CGCGCTCGCGCAGCTGCAGCTGCTCGGCGCCCTCAGTGCAGCTCAGTACCAACCCAGCAGG
 ATGTTGCGAGCTTGGCGCTGGTTTGTGTGGCACTGCAGTGTGATGTGACGGGCGAGCG
 GCCCTCAGCTTCACTGGCACTCCAGATACCCAGTGGCACTTGTGGAGATCACCAACCCCA
 CGCTGGGCATGTATGGGCTGCCCTGCTGCGACCCCTGTGGCCAGCTCCCGACGCGCCTTCC
 AGGCCTTTGCCAATGGACGCTGCTTATCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
 AGCTGCTTACCGGATGAGTACGAGCTGGGCAAGTGCTGAGAGCTCAGTGGACCTGGCATGGCCAC
 CCGCGTGGAGGTTGGTAGGACACACTGGGCGCAGGTTCCATGCAAGCGGTTTGGGGA
 AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAAATGTGGTCATC
 ATCTACCTCAGCGCTGCTGGGAACCTCAGGCTGCAGTCGAGAAGGGGTCTCTGGGCGACT
 GCCCCAGGCGCTGCTCTGCTGCTGCAAGAGCTCTCTCTCTCTCTCTCTCACTCTCTCT
AGCGCCACCCAGGGCTTCCCTAACTCTCCCTTGCCTCTACCAATGCCCTTTAAGTGTGTC
GAGGGGTCTGGGTTGGCAACTCTGAGGCTGCATGGGTGACTTTCACCTTTCTACCTCT
CCTTCTAATCTCTTAGAGACCTGCTATCCCAACTTCTAGACCTGCTCCAACTAGTGA
CTAGATAGAATTTGATCCCCTAACCTACTGCTGCGGTGCTCATGCTGTCAACGATTG
CCTGTGCTCTCTCTCAGGGCGAGCATGCTAACGGGCGACGTCTAATCCAACCTGGGAGA
GCCTCAGTGTGGAATTCAGGCACTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA
ATGAGCTGGGGCTTACGTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGTGG
GAGTAGACAGCTGGCTGGATGGCTCTGAGGCTCCCTGGGGCTGCTCAAGCTCTCTCTGCT
CTTTGCTTTTCTGATGATTGGGGCGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAA
TGTGGGATCTCAGGATGGCTTCTTCTCTTACCTTCTCTCTCAGCTGCACCTCTAT
CCTGGAACCTGTCTCTCTTCTCCCCAATATGATCATGTGTGCTGCTCTCTGCAAAAGGC
CAGCCAGCTTGGGAGCAGCAGAGAATAAACAGCATTTCGTAGCCAAAAA
AAGGCGCGCGCGACTCTAGAGTCGACCT

FIGURE 12

MQELHLLWWALLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPFGFPANVTTLSSLNANRL
 PGLPEGAFREVPLLQSLWLAHNEIRTVAGALASLSHLKSLDLSHNLISDFAWSDLHNLSAL
 QLLKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCCTC
 GIVWLKTWALTAVSIPEQDNIACITSPHVLKGTPLSRLPPLPCSAQSVQLSYQPSQDGAELR
 PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANG
 SLLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPGEGETDLGRRFHGKAVEGKGCYTV
 DNEVQPSGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSTF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites.

amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.

amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,
 334-340, 350-356, 394-400

Amidation site.

amino acids 355-359

Leucine rich repeats.

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain.

amino acids 180-230

FIGURE 13

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACGCCCTGGCTGAGGGAGCTGC
 AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC
 AGCGAGGAGGTCTTGAGCAGCATGGCCCGGAGGAGCGCCTTCCCTGCCCGCGCTCTGGCT
 CTGGAGCATCTCTGTGCTGCTGGCACTGCGGGCGGAGGCCGGCCGCGCAGGAGGAGA
 GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
 CTGATTGTTTTAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAG
 AATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
 CAGAATACTTCTATGAATTCCTGTCTTGCCTCCCTGGATAAAGGCATCATGGCAGATCCA
 ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT
 CCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTGTAAGTGGATGTGATTGTTATGAATT
 CTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCTCTTTAAACATGTCAACAA
 GCTGAGTGCCCGAGCGGGTGCCGAAATGGAGGCTTTTGAATGAAAGACGCATCTGCGAGTG
 TCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG
 GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGT
 GACAAAGCAAAGTCTCAACCACCTGCTTAAATGGAGGGACCTGTTTCTACCTCGAAAATG
 TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAGCAAATGCCACAACCTGTG
 GAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGTCCAAAGGTTACCAGGGAGAC
 CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA
 CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAGGTACGAAGCCAGCC
 TCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGCACACGCCCTTCACTTAAAAAG
 GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACTCCGACATCTGAAAC
 GTTTTAAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTATGTGTTGAATGTTCAAATAA
 TGTTCACTTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
 GATATTTACTCTTCTTTTAAAGTTTCTAAGTACGTCTGTAGCATGATGTTATAGATTTTCT
 TGTTTCACTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAATTTTCACTG
 TGTAGTTGGCAGATATTTCAAATTTACAATGCAATTTATGGTGTCTGGGGGAGGGGAAAT
 CAGAAAGGTTAAATTTGGGCAAAAATGCGTAAAGTCAAGAATTTGGATGTTGTCAGTTAATGT
 TGAAGTTACAGCATTTCAGATTTTATGTGAGATATTTAGATGTTTGTACATTTTAAAAA
 TTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACCTTACCATTATTCAGAGATT
 CAGTATTAACAAAAAATACACTGTGGTAGTGGCATTAAACAATATAATATATCTTA
 AACACAATGAAATAGGGAATATAATGTATGAATTTTGCATTGGCTGAAGCAATATAATA
 TATTGTAACAAAACACAGCTCTTACCTAATAAACATTTTACTGTTTGTATGTATAAAAT
 AAAGTGCTGCTTTAGTTTTTTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

1002796.11504

MARRSAFFPAAALWLWJILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQABEYFYEFLSLRSLDKIMADPTVNVPL
GTPVPHKASVVQVGFPCLGKQDGVAAFEVDVIMVNSEGNTILQTPQNALFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGHPEKEALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICICPPGLEGEQCEISKCPQPCRNGGKICIGSKSKCKSKGYQGDLCSKPV
EPCGGAHGTCHEPNKQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESYIHW

amino acids 1-28

amino acids 88-92, 245-249

amino acids 370-378

amino acids 184-190, 185-191, 189-195, 315-321

amino acids 285-293

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 15

AGAACCTCAGAAATGTGAGTTATTTGGGAATGGCTGTTTGTAATGTCCTTACGTAAGCCAA
GAGGAGGTCTTGACTTGGGGTCCCAGGGGTACCGCAGATCCCAGGGACTGGAGCAGCACTAG
CAAGCTCTGGAGGATGAGCCAGGAGTCTGGAATTGAGGCTGAGCCAAAGACCCAGGGCCGT
CTCAGTCTCATAAAAGGGGATCAGGCAGGAGGAGTTTGGGAGAAACCTGAGAAGGCCCTGAT
TTGCAGCATCATGATGGGCCCTCTCCTTGGCCTCTGCTGTGCTCCTGGCCTCCCTCCTGAGTC
TCCACCTTGGAACTGCCACACGTGGGAGTGACATATCCAAGACCTGCTGCTTCCAATACAGC
CACAAAGCCCCCTTCCCTGGACCTGGGTGCGAAGCTATGAATTACACAGTAACAGCTGCTCCCA
GCGGGCTGTGATATTCACTACCAAAGAGGCAAGAAAGTCTGTACCCATCCAAGGAAAAAAT
GGGTGCAAAAATACATTTCTTTACTGAAAACCCGAAACAATTGTGACTCAGCTGAATTTTC
ATCCGAGGACGCTTGACCCCGCTCTGGCTCTGCAGCCCTCTGGGGAGCCTGCGGAATCTT
TTCTGAAGGCTACATGGACCCGCTGGGGAGGAGAGGGTGTTTCTCCAGAGTTACTTTAAT
AAAGTTGTTCATAGAGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKOL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

FIGURE 17

GCGAGAACCTTTGCAACGCGCAAAACTACGGGGACGATTTCGTATTGATTTTGGCGCTTCGATCCACCCCTCC
 TCCTTCTCTATGGGACTTTGGGGCAAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC
 CAGGACAGGCTCGGGACACAGCACTGGCTCCTGGACCCCAAGATCCTTAAGTTCCTGCTCTCATGCTCGCGG
 TTTCTGCTCGCGTCCGGTTGACTCTGCCACCATCCCGCGGACGACAGTATCCCGACGACAGCTGGCCCCA
 CAGCACAGAGCGCCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAATATACTGGAGCTTG
 TAACCCGTCGACAGAGGGTGTGAATTACACCATTGCTTCCAACAATTTGCCCTTCTTGCTCTATGTGTACAGTTT
 GTAATACAGTCAAAACAATAAAGTTCTCTGTACCACGACGACGAGACCCGTTGTGTGAGTGTGAAAAGGAGAGC
 TTCACGATAAAAACTCCCTCAGATGTGCCGAGCTGTAGAACAGGCTGTCCAGAGGGATGGTCAAGGTGAG
 TAATTGTACGCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAACCCGACGAGC
 CGGAGGAGACAGTGACCACTCCTGGGGATGCTTGCTCTCCCTATCACTACCTTATCATCATAGTGGTTTAT
 GTCATCATTTAGCTGTGGTTGTGGTTGGCTTTTCATGTCGGAGAAATTCATTTCTTACCTCAAAGGCATCTG
 CTCAGGTGGTGGAGGAGTCCCGAACGTGTGCACAGAGTCTTTTCGGCGGGCGTTCATGTCTTACAGAGTTCT
 CTGGGCGGAGGACAATGCCCGCAACGAGACCTGAGTAACAGATACCTTGCAGCCCCACCGAGTCTCTGAGGAC
 GAATCCAAAGTTCAGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCCGAGAGGAGCCACAGCGCTGCTGCT
 GGAACAGGCGAGAAGCTGAAGGGTGTGAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACA
 TCAGCACCTTGTGGATGCCCTCGGCAACACTGGAAGAGGACATGCAAGGAAACAATTCAGGACCAACTGGTG
 GGCTCCGAAAGCTCTTTATAGCAAGATGAGGCGAGGCTCTGCTACGCTCTGCTCTGAAGAAGATCTCTTCAG
 GAACACAGAGCTCTCCCTCATTTGACTTTTCTCCTACAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGA
 CCCATGCCCCAAACAACTCTACTATCCAATATGGGCGAGCTTACCAATGGTCTTAGAGTCTTTGTTAAGCAGCTT
 GGATCAATTTTATGAATACTGCGTGTGATAAGCAACCGGAGAAATTTATATCAGATCTTGGCTGCATAGT
 TATACGATTGTGTATTAAGGGTCGTTTATAGGCCATACGCGTGGCTCATGCCCTGAATCCAGCAGCTTTGATAG
 GCTGAGGCGAGTGGATTGCTGTAGCTCGGGAGTTTGAACAGCCTCATCAACACAGTGAATCCATCTCAAT
 TTAAGAAGAAAAAGTGGTTTATAGGATGTCATTCTTTGCAAGTCTTTCATCATGAGACAGTCTTTTTCGCTG
 TTTCTATATTGCAAGCTCCATCTCTACTGGTGTGTGCATTTAATGACATCTAATACAGATGCCGACAGCCAC
 AATGCTTTGCCCTATAGTTTTTAACTTTAGAACGGGATTTATCTGTTATTAACCTGTAATTTACGTTTCGGGATA
 TTTTGTACTTAATGATGAGATTATCAAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTC
 GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTTGGGCTTACCCCCACCTTAATAGAGAAACATTTATATTG
 CTACTACTGTAGGCTGTACATCTCTTTCCGATTTTGTATATGATGATAAATGGAAPACCTTAGGAAAT
 GCATTTATAGGCTGTTTACATGGTGGCTGGTATACAAATCAGCAGTCAAAAATGACTAAAAATATAAGTATG
 GACGAGGGAGGAAATCCTCCCTCTGTGGGAGGCATCTACTGCATTCAGTTCTCCCTCTCGCGCCTGAGACTG
 GACCAGGGTTGATGGCTGGCAGCTTCTCAAGGGGAGCTTGTCTTACTTGTATTTTATAGGCTTATATAGCCA
 TATTTATTTATAAATAAATATTTATTTATTTATTTAAGTAGATTTTACATATGCCAGGATTTTGAAGAGC
 CTGGTATTTTGGGAAAGCATGTCTCTGGTTTGTCTGCTGGGACAGTCAAGGACGTCATCTCCGAGTCTTGC
 CACAGCAGATGAGGACAGTGAGAATTAAGTTTATAGTCCGAGCTCGGAAGAGCTCTCTTCTCAAGCGCCATTACA
 GTTGAACGTTGATGAATCTTGACCTCATTTGGGCTCAGGCGAGCAGGCTGTTATCTGCCCGGCATCTGCC
 ATGCCATCAAGAGGAGACTGCAGCGTGGTGGGAATGGCTGAATGGTGGCGACTCAGCATCGATGCGTGG
 CCGCTTCGCTCTCGTGGTCTGTGAAGTCACTCCCTGGGATGCCCTTTTGGGACGAGATTCTCTGAGCTGCGTTT
 TATGGTACAGATTCCCTTTTGAAGACTTGGCCCTCTGAAGCATCTGACTCATCTCAGAGATTCATCAATCT
 TAAACACTGTGACACAGGATCTAAATAGGCTGACACATTTGCTGTGTGTCAGTTCGATTTATTTATTTAAA
 AACCTCAATATCTGTTTAGCTCTCTTCAGCAAACTCTCTCCACAGTAGGCCAGTCTGTTGAGTATATATTTAAA
 CGGATATAGCTATCTTAGGGTTTTCAGTCTTTTCCATCTCAAGGCATTTGTGGTTTGTTCGCGGACTGGTTG
 CTGGGACAACTTAGACACTGCTGAAGTTCGCACATTCAGATTTGTGTGCTCATGGAATTTTAGGAGGGATG
 GCCTTTCCGGCTCTCGCATCTCCATCTCTCCACCTTCCATCTGGCGTCCACACCTTGTCCCTGTCACTTCTG
 GATGACACAGGGTGCTGCTGCTCTAGTCTTTGGCTTTGCTGGGCTCTCTGTGCGAGGAGACTTGGTCTCAAG
 CTCAGAGAGAGCCAGTCCGCTCGCCAGCTCCTTTGCTCCTCTCAGAGGCTTCTTGAAGATGCTCATAGACT
 ACCAGCCCTTACAGTTTAAAGCTTATTCCTTAAACATAAGCTTCTGACAACTGAATTTGTGGGGTTTATTT
 GCGGTTGTTGATTTGTTAGGTTTGTCTTTATACCCGGGCCAAATAGCACATTAACACCTGGTTATATATGAAA
 TACTCATATGTTTATGACCAAAATAAATATGAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVVFIVAVLLPVRVDSATIPRQD
 EVPQQTVAPQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
 QTNKSSCTTTTRDTCVQCEKGSFQDKNSPEMCRTCTGCPRGVMKVSNCNCTPRSDIKCKNESAA
 SSTGKTPAAEETVTTILGMLASPHYHLIIIVVLVIIILAVVVVGFSCRKKFISYLGKICSGGG
 GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAEITGVTVES
 PEEPQRLLQAEAEGCQRRRLVVPVNDADSADISTLLDASATLEEGLHAKETIQDQLVGSEKL
 FYEDEAGSATSCSL

Important features of the protein:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

FIGURE 19

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAAG
TTTATTAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTCCGAAATT
CAGAGAGAAAAGATCAACCACCTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATCTTAAAAAAAAA

FIGURE 20

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSWGP AEIQIEGCIPKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FIGURE 21

CCGGGGAGGGGAGGGCCCGTCCCGCCCCCTCCCGTCTCTCCCGCCCCCTCCCGTCCCTCCC
 GCCGAAGCTCCGTCCCGCCCCGCGGCGGCTCCGCCCTCACTCCCGCGCGGGCTGCCCTC
 TGCCCGGGTTGTCCAAGATGGAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG
 TTCGTGGCGCTACCCGCTCCGGCTGGCTGACGACGGGCGCCCCGAGCCGCCGCCGCTGTC
 CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACTACACTGAAAGATGATGGGGACATAT
 CTAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA
 CCTGTAAATAGTGGTGTAAACCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT
 TGAAAATTTGGAGGAAAAAGAATATTTTGAATTGTCAGTGTAAGGATTTTAGTTCATGAGT
 GGCCTATGACATCTGGTTCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
 GATGGAAAACAAGTTCAGCAAAAGGATGTCAGTCAAATTGATATTTTAGTTAAGAACCGGGG
 AGTACTCAGACATTCAAACTATACCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC
 GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCAAAAAAGAAAGTGTAGTTCACTG
 CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAACCACTGTAGATGAAGATGTTTACC
 TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC
 AGTGGATGGAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC
 TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
 AAAGGTGTTTTTCCAGTTTTCTGAATACAAAGGAATTCCTCAGTTGGATAAAGTGGACGTCA
 TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
 GATAAACATGTATTTAAACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC
 AAATTGCCACTTGAATATAATTTTCTTTAAATCGTT

FIGURE 22

```
>>/usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA60783
>>subunit 1 of 1, 330 aa, 1 stop
>>MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVVLNITYESGQVYVNDLPVNSGVTRISCQTLLIVKKNENLENLEEKEYFGIVSVRILVHEWPMTSSSLQLIVIQEEVVEIDGKQVQKQDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRSDSILFTLPNLNKKESVSSLQTTSTQYLIRNVETTVDVDLPGKLPETPLRAEPPSSYKVMCQWMEKFRKDLCRFWSNVSPVVFQFLNIMVVGITGAAVVITILKVFFPVSSEYKGILQLDKVDVPIPTAINLYPDGGEKRAENLEDKTCI
```

Important features of the protein:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCGTTTCGCC**ATG**CGTCCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGG
 CCTCGGCTTGGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGTGGT
 GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCTC
 CGGGCCGAGTGCTGTGCTCCGGCAACATTGACACCGCCTGGTCCAACTCACCACCCCGG
 GGAACAAGATCAACCTCCTCGGCTTCTTGGGCTTGTCCACTGCCTTCCCTGCAAAGATTG
 TGCAGCGGCGTGGAGTCCGGCCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGTG
 CGAGTGCGCCGCCGACTGCTCGGGGCTCCCGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG
 CCACCTACCGCGCAGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGC
 GTCATGTATCCGGGGCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTC
 GTGCGTCGTGGACCAGACGGGGCAGCGCCCACTGCGTGGTGTGTCGAGCGGCGCCCTGCCCTG
 TGCCCTCCAGCCCCGGCCAGGAGCTTTCGGGCAACAACACGTCACTACATCTCCTCGTG
 CACATGCGCCAGGCCACCTGCTTCTTGGGCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG
 CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAAGTTCGT**GT**
GAGCCTGCAGGACAGGCCCTGGGCTGGTGCCGAGGCCCCCCATCATCCCTGTTATTATT
 GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCTTAGAGCCCGGATTTCGGACCACTT
 GGGGATCCAGAACTCCTGACGATATCTTGAAGGACTGAGGAAGGGAGGCCCTGGGGGGC
 GGCTGGTGGGTGGGATAGACCTGCGTTCGGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT
 AGGATCCCCAGCCCTACCTAAGACCTATTGCCGGGAGGATTCCACACTTCCGCTCCTT
 TGGGGATAAACCTATTAATTATTTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGTTAAT
 CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGACGGAGGGT
 CTAGCCTGGGTGTGACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG
 TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG
 CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
 GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
 GGTGAGTATGGAGGGTCTAGCCTGGGTGTGACGGAGGGTCTAGTCTGAGTCCGTGTGGGA
 CCTCAGAACACTGTGACCTTAGCCACGCAAGCCAGGCCCTCATGAAGGCCAAGAAGGCTGC
 CACCTTCCCTGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
 CCTGTGAAGGCCATTGAGAAATGCCAGTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCC
 TGACACGGGTGTGCTTGGCCACAGAACCCACGCGTCTCCCTGCTGCTGTCCACGTGAG
 TTCATGAGGCAACGTGCGGTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGC
 ACTGTGTCGGCGGGAGCCAACTCCACTCTGGGGGAGCTTGGCGGGGACCACGGGGCCACTGC
 TCACCCACTGGCCCCAGGGGGGTGTAGACGCCAAGACTCAGCGATGTGTGACATCCGGAGT
 CTTGGAGCCGGGTGCCAGTGGCACCACCTAGGTGCTGCTCCACAGTGGGGTTACACA
 CCCAGGGCTCCTTGGTCCCCACAACCTGCCCGGGCCAGGCTGCAGACCCAGACTCCAGCC
 AGACCTGCCTCACCACCAATGCAGCCGGGGCTGGCGACACCAGCCAGGTGCTGGTCTTGGG
 CAGTTCTCCACAGCGCTCACCCTCCCTCCATCTGCGTTGTAGTCTCAGAATCGCCTACC
 TGTGCCCTGCGTGTAAACACAGCCTCAGACCAGCTATGGGGAGAGGACAACACAGGAGGATAT
 CCAGCTTCCCCGCTCTGGGTGAGGAATGTGGGGAGCTTGGGCATCTCTCCAGCCTCCTC
 CAGCCCCAGGCATGCTTACTGTGGTGCCCAAGTAAGTGCCTTAGGTTGGTGGGTCTA
 CAGGAGCCTCAGCCAGGCAGCCACCCACCTGGGGCCCTGCCTCACCAGGAAATAAGAA
 CTCAGGCATAAAAAAA

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGFVSSMGSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAECCL
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEHVVCPRPQSCVVDQ
TGSAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

FIGURE 25

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGT
 TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT
 AAAATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAA
 ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCCGCCTGGCTA
 CCATGATGGTGCAGGGCAAGAATACGAGGCAGGAGGTTCTGTCTCATCCATCCTTTAAATCTG
 CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTCAGGCCTCTGGTGGCCTACT
 GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA
 TTAATTAGTTTGGCGCTATGGATTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTG
 TTAGACAAGTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTGCGA
 AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGGAAATGCTTAATCGAACACTTCTTG
 AAACCTTGCAAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG
 AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGGCGGTGTCACTGTCTCTG
 TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTGTTGCTCAGGGCTTCTGC
 AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAAACAAAGACC
 AAGTACACAGGAAATCCAACAAGATGTATGAAGTGGTCTACCAATTTGGAAGTGAAGTGTG
 TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTGAATCGAAAAATGTGCAATATTA
 CTTTCTCAACTTTGATCCTCCAATGAGGAATCCATCAATATTATCAACATATAGTGACA
 ACTTTAGTTAAGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTTGG
 CCTTAATACAGTTTTTAACCACTGATAATTCAGATTTGTTCAATACAGTATTGGGATTGTGC
 CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGAAGATC
 TTTTCCCAAGAACTCTTACTAAAGCACAAATTTAAAGCTCTTCTGTCTTATGATTATGC
 TGTGAAGAAGCCATGGCTTGCAATCCTCACTATAAGCCCCGGAGAAATGCCCTCTATCA
 TTCTCCATGATCGACTTATTACCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATG
 AGTGCCATTGCAGCCCAACGCTGCACTCCTTGCCATCACCGTGGAACGGGCACACAGA
 CATGATTGATCAGGATGGCTTATATGAGAAACTTAAACTGAACATTGAAGTGACACACTCC
 TTTTCCCTCCTAGTTCCAAATGACTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGA
 TGATTTTGAACAGATATTTTGCCATTATCATTGTTTAATAAAAGTAATCCCTGCTGGTCAT
 AGGAAAAAAAAAAAAA

FIGURE 26

amino acids 12-23, 232-243

FIGURE 27

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGAT
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTGCCCAAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCAGTCAGAGCTATAA
GAGATGATGGAAAAAGCCTTCACCTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAATAAATGTTTTTTAAATCTGA

28/75

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIKKEKRPQTLSRGWDDITWVQTYEEGLFYAQSKKPL

MVIHHLEDCQYSQALKKVFAQNEEQEMAKNFIMLNLMHETTDKNLSPDGQYVPRIMFVDP

SLTVRADIAGRYSNRLTYEPRDLPLLIENMKKALRLIQSEL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation site.

amino acids 51-57

1000795.11501

FIGURE 29

TAAACAGCTACAATATTTCCAGGGCCAGTCACCTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCGCCCACTTCCAC
CAATTCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCTTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

JUL 27 1975 11:50

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9700, pI: 9.55, NX(S/T): 0

MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFP
WFRRNFPPIPIESAPTTPLPSEK

Important features of the protein:**Signal peptide:**

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

GGGACGCGTGGGGCGGCGCGCCGGGAGGACCGCGCGCGGCATGGCGCCGGGGGGCCCTGGGAT
GCGGGCCCCCTCTCGCCCGCCTGCTGCCGCTGTGTGCTGTCTGCCCTGGCGCCGCGCGCGCG
GGGAGCGCGCGGGCCCGGCGGTTCAGCTGTTCGTCATCTGCCATGCAACATGCCACATCGC
AGCAAGAAGGAAGGGAAGAAGATCTGTATTTTGCAACTATGGATTTCTAGGGAACGGGAGGACT
CAGTGTGTTGATAAAAAATGAGTGGCAGTTTGGAGGCCACTCTTGTCTGTGGGAACACACATC
TTGCCACAACACCCCGGGGCGCTTATTGCACTTTGCCTTGGAAGATATCGAGCCACAACA
ACAAACAGACATCTATTCCCAACAGTGGCCACTTTTGTACAGACATAGATGATGTGAAGTT
TCTGCCCTGTGCAGGCTATCGAGGCGATCGCTGAACACTCATGGAGCTTTGAATGCTACTC
TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCGGACCACCGATGCCACA
CATGACAGAAAATAGACTGTGTGTAACCTCTGAGGTTCGAGATGGCTATATCATAGGAAT
TATAGCTCTAGCTCTGGGACGCGAGGTTCGTTATGCTTGACAGAAGAGATCTTCACTGTTC
AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC
AAGAGATCAACTGTGGCAACCCCTCCAGAAATCGGGCAGGCCATCTTGGTAGGAAATCACAG
TCCAGGCTGGGCGGTGTGGCTCGCTATGCTGTCAAGAGGCGTTTGAGAGCCCTGGAGAGAA
GATCACTTCTGTTTGCACAGAAAGGCCACTGCAGAGAAAGTACTTTAACATGCACAGAAA
TCTCGACAAGAAATTAATGATGTATCATCTGTTTAATGATACCTGTGTGAGATGGCAATAAAC
TCAAGAAGAATAAACCCCAAGATCTCATATGTGATATCCATAAAGGACACCGGTTGGACCC
TATGGAATCTGTTCTGAGGAGACAGTCAACTTGACACAGACAGAGACCCCAAGAAGTGT
GCCTAGCCCTGATCCACGGACCAACTACACCGTGAACATCTCCACAGCACTCCACGGCGC
TCGATGCCAGCGGTCTATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGAAG
TTTCAATATTTCAATATTTAATGAAGACTTGTGTGAATTTGAACAGGCGGTTCTAGGAAGTTG
GATCAAGACACATGTACCAATTTACCGTTCTGGGTCAAGGTTGGTATCTTGCTCATCTTCT
CATGCAACATCTGTTTAACTTCAACAGGGAACAAGTGCCTGTAGTGTGTTTGGATCTGTA
CCCTACGACTGATTATACGGTTGAATGTGACCTGCTGAGATCTCCTAATCGGGCACTCATGTC
AAATTAACATAGCAACTCCCCAGCAGTAATAACAGACATCAGTAACATTCAGGATTTAAT
GAAACCTGCTTGAGATGGAGAGCACTCAAGACAGTGTATAGGAGAGATGTATTTATTCCA
CATTTGGGGCGAGAGATGGTATCAGAAGGAATTTGCCAGGAATGACCTTTAATATCAGTA
GCAGCAGCCGAGATCCCGAGGTGTGCTTGACCTTACGTCGGGTACCAACTACAATGTCAGT
CTCCGGGCTGTGCTTGCGAACTCTCTGTGTCATCTCCCTGACATCCACAGATACAGAGCC
TCCCCTCCGGAAGTAGAATTTTTTACGTTGCACAGAGAGCTTACCCAGCCCTCAGACTGA
GGAAAGCCCAAGGAAGAAAATTGACCAATCAGTTCATATCAGGTGTTAGTGCTTCCCCTGGCC
CTCAAAGACACATTTTCTGTATTCTGAAGCGGCTTCCCTCTTCTTAGCAACGCCCTCTGA
TGCTGATGGATACGTGCTCGAGAACTATGGCCAAAGATGTCCAGATGATGCCATGGAGA
TACCTATAGGAGACAGGCTGTACTATGGGAAATATATATGCAACCTTGAAAGAGGGAGT
GATTACTGCTATTATACGAATCACAAGTGAATGGAATAAGGTGGAAGACACTCTCTGTGC
AGTTTGGGCTCAGGTGAAAGATTCGTCACTCATGCTGCTGCAGATGGCGGCTGTGGACTGG
GTTCCCTGGCTGTGTGATCATCTCTCATCTCPTCCTTCTCAGCGGCTCGATGGCAGATG
GACACTGAGTGGGAGGATGCACTGCTGCGGACGGTTCTTGGCAGCTTCTCAGGTGCC
GCACAGAGGCTCCGTGTGACTTCCGTCCAGGGAGCATGTGGGCGTCAACTTCTTCCATTC
CAGCTGGGCCCCATCTCTGTAATTAAGATGGTGCTATCCCTGAGGATACCAATAAGGAGA
AAACTCAGGAATTTCTAGTCTTCCCTGCTACAGAGCAAGCTTGTGCAATGAACATAGACT
CCTGATGTACATGTGATATGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC
TTCTCTGTAGTGATGCTTGAGGTCAGCTCCTCTAGACATGTAAGTCAAGGAATCTCTGCA
ACCTCCTATATAAAAGCAATTTCTGTATTAATCATTCAGAACTCATTTTATAAATGCAAGT
AGATGGGCTTAAGTTTGGCTAGAGTTTGAATTTAGAGGAGGCTATTGAAAAGAGACA
GTACGCTAGGCAAAATGTTTCAAGCACTTTAGAAAACAGTACTTTTCCATATTAATTTGATGAT
ACTAATGAGAAAAATACTAGCGTGCCATGCCAATAAGTTTCTGCTGTGCTGTTAGGCA
GCATTCGTTTGTATGCAATTTCTATTGTCTTATATATTCAAAGTAATGTCTACATTCAGTA
AAAAATCCCGTATAAAAAA

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPSRRLPLLLLLGLARGAAGAPGPDGLDVCATCHEHATCQOREGKKICICNYG
FVGNRGRTQVCQDKNCEQFGATLVCGNHTSCHNTPGGFFYCICLEGYRATNNKTFIPNDGTFCT
DIDECEVSGLCRHGGRCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATEIDCGTPPEVP
DGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTWESPKLHCQEINCGNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFESPGGKITSVCTEKGWTRESTLTCTEILTINDVSLENDT
CVRWQINSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTEPVCLALYPGNTYTVNI
STAPRRSMFPAVIGFQTAEDVLLLEDDGSFNISIFNETCLKNRRSRKVGSEHMYQFTVLGQR
WYLANFHSATSFNFTTREQVPVVCCLDLYPTTDTYVNVITLLRSPKRHSVQITITPPAVKQTI
SNISGFNETCLRWSIKTADMEEMYLFIHWGQRWYQKEFAQEMTFNISSSSRDPEVCLDLRP
GTNYNVSLRALSSSELPVVISLTTQITEPPLPEVEFFTVHRGFLPRLRLRKAKEKNGPISYQ
VLVLPALQSTFSCDSEGAFFFFNASADAGYVAAELLAKDVPDDAMEIPIGDRLYYGEYYN
APLKRGSQDYCIILRITSEWNKVRHSCAVWAQVKDSSMLLMQAGVGLGLSLAVIILTFLSF
SAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 718-740

N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352,
367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474,
498-502, 503-507, 542-546, 563-567, 645-649

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

Tyrosine kinase phosphorylation site.

amino acids 419-427

N-myristoylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126,
146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694,
727-733.

Amidation site.

amino acids 52-56

Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

Cytochrome c family heme-binding site signature.

amino acids 39-45

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 85-106, 135-156

Receptor tyrosine kinase class V proteins:

amino acids 389-422

1002795.11501

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCGACCCGCGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCAGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGCGCTCAACCCAGCCGCGCCCATTCAGAAAGCAGAGACCAGGGGAGCCAA
GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTACAAAAACATCTCCCACTTCATGGTGC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCAGAGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCTGTCTCTAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCAAAAACATCGAG
GTTATTAATTGCAGCATCAGAGAAATAGAAACAACAACTTCCAGCATCCCTGGGGCTCAGA
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCTCGTCCACCTCCGATCCACCAGCTCTGC
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC
ACAGCCGGCACCCAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTC
CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCTCGGAAGCCGCCCTCAAGAACCTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCTT
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCACAGAC**TGAG**TGCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCCTTACTCGTGTGAGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
GGCCCCCACCAGAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCAAGCCCTTAACCCAGATGTGGCAACAGGACCTTCGCTCACATCCAC
CGGAGTGTATGTATGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
CACATGTTCTGTGTTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA
TTAAATTCACTCAGTGTGGCCCAAAAAA

FIGURE 34

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALLETQTLSA
ETSSRASTPAGPIPEAETRGAKRISFARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
TTVQITITGSDPEAIFDTLCTDDSSSEAKLTMTDILTIAHTSTEAKGLSSESSASSDGHFV
ITPSRASESSASSDGHFHVITPSRASESSASSDGHFHVITPSWSPGSDVTLLEALVTVTNI
EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAE TL
STAGTTEASAAPHATVGTPLPTNSATEREVAPGATLTSGLALVTSRNPLEETSALSVE TPSY
VKVSGAAPVSIEAGSAGVKTTTSFAGSSSVPSEAKLNKFTPSRPTMDIATKGFFPTSRD
PLPSVPPTTNSRGTNSTLAKITTSAKTTMKPOOPRPLPGRGRPT

amino acids 1-25

amino acids 252-256, 445-449, 451-455

amino acids 84-88

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
314-320, 349-355, 386-392, 397-403, 449-455

amino acids 385-393

FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCGGCTCTGACAGCCACTCCAGAG
 GCCATGCITTCGTTTCTTGCCAGATTGGCTTTCAGCTTCTCTGTTAATTCCTGGCTTTGGGCCA
 GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
 CCCAGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAAATTTCCAGGATCGCGAGGCAGCA
 GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT
 ACTTCGCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
 CCTGCCTGCAGAAGCTCCTCTACTTTAACCCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
 TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA
 ACTGGCTCTGTTCTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
 AAATGTTTGTGTGCGGTGAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT
 GTAGCTAAGGATTGGAATGACAACCCCGGAAAAATTTGCGGTATTCTCTGGAGATACTGGT
 CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
 GCTCCCTTCATGCTTCCCTGCTGGTGGTGAATCTCAACCTGATCAGTGCCACCCCTTCTCGG
 AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTGTGCCACCGTCACCA
 GCTATTTCATTAACCTCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTCA
 TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT
 TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT
 CCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC
 GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGGTAGGATGTGAGAAATGGGAAT
 AGAAGGAGTGTCTTAGGGTAAATCTTTTAATAAACTACCTATCTGTTTATGACCACCTTA
 GATCGAAATGTC

MLRFLPDLAFFSLLILALGQAVQFQEEYVFLQFLGLDKAPSPQKQFQVPVYILKKIFQDREAAA
TTGVSRLDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTPKPGKMFVLRSPVPQGAHVFNLLDV
AKDWNPNPRKNFGLFLEILVKEDRDSGVNFQPEDCTCARLRCSLHASLLVLTNPNPDQCHPSRK
RRAAIPVPLKSCNKLNRHQLFRINRDLGHWKIAPKGMVIANCHYCGEFPSTLSLSSNY
AFMOALMHAVDEPIPOACVITPKLSPISMLYODNNNDVILRYHEDMVVDECGCG

Signal peptide:

N-glycosylation sites.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

N-myristoylation site.

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

FIGURE 37

CACTTCTCCCTCTCTTCCTTTACTTTTCGAGAAACCGCGCTTCGGCTTCTGGTCGCAGAGAC
 CTCGGAGACCGCGCGCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
 CCGCGCCCCACCTCTCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTCTGCTCTGTT
 TCCTTACCCGAGTCTGTGCATCGCCCCGAGCTTGGCCGGGAGGAGGCTTGGCGCGCGGAGAGA
 TGCTCTAGGGGCGGCGCGGGAGGAGCGCGCGGGACGGAGGGCCCCGGCAGGAACATGGGCG
 TCCCGTGGACAGGGACTCTTGTGTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT
 CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCACTCAG
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGGCGCTGCTGTGACCCCGGTACCTCCATGTACCC
 GGCACCGCCGTGCCCCAGATCAACATCACTATCTTTGAAAGGGGAGAGGGGTGACCGCGGAG
 ATCAGGGCTCCAAGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
 CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGGCGGGAAGGCCCATGCACAGCAACCCTACTACCAGACGGTGATCTTCG
 ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGCTAC
 GTGCCCGGCTCTACTTCTTACGCTCAACGTGCACACCTGGAACCAAGAGGAGACCTACTCT
 GCACATCATGAAGAACAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTTGGGCGACCGCAGCA
 TCATGAAAAGCCAGAGCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCCTC
 TACAAAAGGCGAAGCTGAGAACGCCATCTTACGGAGGAGCTGGACACCTACATCACTCTCAG
 TGGCTACCTGGTCAAGCAGGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
 ACCTTCCACCCCTGCGGTGTGCTGACCCACCGCCTTTCGCCACTCCCTGGACTCCGACTC
 CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
 CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGACCCGCG
 GAGAACCCTCTGGGACCTTCGCGGCCCTCTCTGCACACATCTCAAGTGACCCCGCACGGC
 GAGACCGGGTGGCGGCAGGGCGTCCCAGGGTGGCGCACCGCGCTCCAGTCTTGGAAATA
 ATTAGCCAATTTCAAAGCTCTCAAAGGAGCAAAAGTAAACCGTGGAGACAAAGAAAAGG
 TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCCTTTTCACTTGAG
 ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG
 AAACCTACCTCTGGCTTAATTTCTTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC
 CTGACATCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTTCTGAGTCAAGCTGCGAGGT
 TAGGGGGCTGGGGCCCCAGGCGCTCAGCCTCCGAGAGGGACAGCTGAGCCCCCTGGCTGGC
 TCCAGGTTGGTAGAAGCAGCGCAAGGGCTCTCTGACGTGGCCAGGACCCCTGGGCTCCCCCA
 GGCTGCGAGATGTTTCTATGAGGGGCGAGAGCTCCTTGGTACATCATGTGTGGCTCTGCTCC
 ACCCTGTGCCACCCAGCAGGCCCTGGGGGTGGTCTCCATGCTGCCACCTGCCACCTCGGCTCGGT
 TTCTGTGCCGCCCTCCACACAATCAGCCCCAGAAGGCCCGGGGCCCTTGGCTTCTGTTTTT
 TATAAAACACCTCAAGCAGCACTGCACTCTCCATCTCCTCTGTGGGCTAAGCATCACCGCTT
 CCAGCTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCCACTGCCCT
 CATCCAGGCTCTGACCACTAGCCTGAGAGGGGCTTTTCTAGGCTCTCAGAGCAGGGGAGAG
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTGT
 AGACAGAGTCAAGAGGAAGTACAGTCCCAATCACCGTGTCCAGGATTCATCTCAGGAGC
 TGGGTGGCAGGAGAGGCAATAGCCCTCTGGCATTGCGAGCAGGCTGGAGCAGGGTTGCG
 GTGCTCTCACGGTGCTCTCGCCCTGCCATGGCCACCCAGACTCTGATCTCAGGAACCC
 ATAGCCCCCTCCACCTACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGGC
 CCCAAACCCCGCTGCTCTCTCTTCCCTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC
 TTCCCTCTCTGGCCTGGCTGCCGGGATCTGGGTCCTTAAGTCCCTCTCTTTAAAGCACTT
 CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
 GCTGCTTAAGCTCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGRLQGKYGKTGSAGARGH
TGPKGQKGSMPGAPGERCKSHYAAFVSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDERSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA
 GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGACATGGGCTG
 CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCCTGT
 GACACTCAAGAGCTACGATGTCTGTGTATTCAGGAACACTCTGAATTCATTCCTCTCAAAC
 CATTAATAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG
 TCCCAAAAAATGGGAGTATGATTTGTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT
 GGCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT
 GAAGCTTCTGTATAGTGTGAGCATGAAAAGCCTCTATATCTTTCATTTGGGAGACCTGAGA
 ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
 AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCCTA
AAAGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTGGCGTTCTCA
 TTCTTATACTCTATTTCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
 TATTATAAATGTTTTATTACTTAACTCCTAGTGAATGTTACAGGTGACTGCTCCCCCAT
 CCCATTTCCTTGATATTACATATAATGGCATCATATACCCCTTTATTGACTGACAACTACT
 CAGATTGCTTAACATTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
 TGCATCTCGGTGTAGAGCAAGGCTCCTTGCTTCAGTGCCCCAGGGTGAATACTTCTTTGA
 AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSFIPLKLIKINIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

10002795.11501

FIGURE 41

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCCAAGTACAGCCAAAGGAAGAT
TCCCCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCAGGG
CTGCAGGAAGGACAGGGGGGCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAGGCTGCA
AGAGGACTGAGCGGTACAGACCCCTAAAGGGCCATAGCCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACCAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGGAGAGTCTCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCCT
TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT
TGTAATATGATTATACCTAACTGAATAAAAAGCTGTCTGTCTTCCNCCA

FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLLILVLAFIGIPRTQSGDGAQDCLKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFLPRKRKSQAEKLCADPKELWVQQLMQHLDKTSPQKPAQGCRKDRGASKTGKKKGSGKCKR
TERSQTPKGP

Important features of the protein:

Signal peptide:

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCGTATTC
 CACAGACATGCACCATATAGAAGAGAGTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
 ACACCTTCCCAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
 GATGTGTGCTGCGTGACCAAGAACCCTCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
 TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACCTTTTCTCTACA
 TGCAGAAAACCTCTGCGGCAATGTGAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
 AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
 ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
 CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
 GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGAAGGCCCTTGACAGCTGAAAGTCC
 CACTGGCTGGCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
 TTGTAATAAACTCTATCTGCTGAAAGGGCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
 CCCATCTAATTTATGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
 GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGPTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMOKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

1002735.1.txt

FIGURE 45

GCTCCCAGCC**AAGAAC**CTCGGGGCCGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG
 CTAAGCGAGGCCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGGCGGGGTACCCCGGCTGGGA
 CAAGAAGCCCGCCGCTGCCTGCCGGGGCCGGGGAGGGGCTGGGGCTGGGGCCGGAGGCCG
 GGTTGTAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGACCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTGGTGGTCCACGTATGG
 ATCCTGGCCCGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACCGGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTCGGGCACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCCGCGCATCCGTGCCGACGGCGTCTGTGGACTGCGCGCGGGG
 CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
 CGTGACAGCGTGCAGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
 AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG
 GACCCATTGGGGCTTGTACCCGACTGGAGGCGGTAGGAGTCCCAAGCTTTGAGAAG**TA**ACT
 GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCTGAGTCCAGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGTACATATTAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
 CATACATTTGAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA
 GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGTTGAATACCTCCATCGATGGGGAAC
 TCACTTCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTCAAGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAAGTGAAGTGGAGCAGGCATGGCCACAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAAGTTGAGAATTCCCC
 CTGAGGCCAGTTCTGTATGGATGCTGTCTGAGAATAACTTGCTGTCGCCGGTGTCACTGC
 TTCATCTCCAGCCACCAGCCCTCTGCCCACTCATATGCCTCCCCATGGATTGGGGCCT
 CCCAGGCCCCCACCCTTATGTCAACCTGCACCTCTTGTTCAAAAATCAGGAAAAAGAAAGAT
 TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAG
 CCTTTCCAGCACTTGGTTTTCCAAACATGATTTTATGAGTAATTTATTTTATATGTACATA
 TCTCTATTTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG
 TTTGTATATTAAATGGAGTTTGTTGT

FIGURE 46

MRS GCVVHVH WILAGLWLAVAGRPLAFSDAGPHVHYGWGDFIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVLRRTVAIKGVH SVRYLCMGADGKMQGLLYSEEDCAFEE
EIRPDGYNVYRSEK HRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDFFGLVTGLEAVRSPSEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

1006795.1101

GTCTGTTCCCAAGGAGTCCTTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGATGGGACAAATGGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCATTGGGCAGTGTTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTGAAGTTGTCTGTGCTACTCTGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCTATGTCTCTGAATCCCAACAGGAGAGCTGGTCTTTGATCCCTGTGACCTCTGATACTGGAGAATAAGCTGCTGTGAGCGACCGAATGGGTATGGGACACCCATGACTTCAAAGTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGCTCATCGTGGCAGCCGCTCTTGTAACCTGATTCTCTCTGGGAATCTTGTTTTTTGGCATCTGGTTTGCTATAGCGGAGGCCACTTTCAGAGAACAAAGAAAGGGACTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCTCTGGTGTGACGCTGGTTCGCGCTACCCGCTATCATCTGCATTTCGCTTACTCAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTTACACCCACAGGGCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCTCTCTCATGCCCTCCCTCCCTTCTCTACCCTGCTGAGTGGCTGGAACCTGTTTTAAAGTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTTCCCTCTAAGTAGACAGCAAAATGGCGGGGTCGAGGAATCTGCACTCACTGCCACCTGGCTGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTCTCTGTGTACTGACGACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCTTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAAGCTGAAGCCAAAAGGATTTAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGGCGCAGTGGCTCACGCCCTTAATCCCAGAGGCTGAGGCGAGGCGGATCACTTGAGGTGGGGATCTGGGATCAGCCTGACCAACATGGAGAAACCTTACTGGAATAACAAGATTAGCCAGGCATGGTGTGTCATGAACTGAGTCCAGCTGCTCAGGAGCTGGGCACAAAGAGCAAACTCCAGCTCAAAAAAATAAAAAA

FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSLAYSGFSSPRVEW
KFDQGDITRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPSEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 49

CCCACGCGTCCGAACCTCTCCAGCG**ATGG**GAGCGCGCCGCTGCTGCCAACCTCACTCTGT
 GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTAGTACGTGAGGGACAGGGCGCCATGACC
 GACCAGCTGAGCAGGGCGAGATCCGCGAGTACCAACTCTACAGCAGGACCAAGTTTGCCAAGC
 CGTGCAGGTCAACGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
 TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
 TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG
 CGTGTTACGGAGATCGTGCTGGAGAACAACATACGGCCTTCCAGAACGCCCGGCACGAGG
 GCTGGTTCATGGCCTTACAGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
 CAGCGCGAGGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC
 CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCGCCGGACCAAGCGCACAC
 GCGCGCCCCAGCCCCCTACG**TAG**TCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCC
 CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
 GAGGGAGGACCTTGAGGGCCGCAAGCATCCGAGCCCCAGCTGGGAAGGGGAGGCCGGTG
 CCCAGGGGGCGGCTGGCACAGTGCCCCCTTCCCGAGCGGGTGGCAGGCCCTGGAGAGGAACT
 GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCGGCCTCCCAGCCGGGCTCCTGAAGCC
 CGCTGAAAGGTGAGCGACTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
 TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
 GGAAGGGACTTTTGTGTTGTTGTTGTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAAATAG
 AGGGTTGTCCACTCCTCACATTCACAGCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
 CGGAATAAAACCATTTTCCTGC

FIGURE 50

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKF AKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQNA RH EGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHA EKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

100079-11301

FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
 TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAAGAAAGAAAGA
 AAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTGGGCAATCTTCAC
 GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
 CCAAAGCTATGGACAACGTGACGGTCCCGCAGGGGAGAGCGCCACCCTCAGGTGCACTATT
 GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
 CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
 AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
 CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATTTC
 TTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
 CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
 GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATATCCACCATACA
 TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
 TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
 GAAAGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAACTCATCTTCTCAATGTCTCTG
 AACATGACTATGGGAACACACTTGCGTGGCCTCCAACAAGCTGGGCGACACCAATGCCAGC
 ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
 CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
 ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACACAGCAATGGCAACAC
 CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
 AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAGAAATTGAA
 AATTGCCTTGAGATATTTAGGTACAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGC
 ACACCCGGCTTGAGCCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
 GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCGAGCTGGCCATCCCA
 AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGCGCTGCGG
 GCACCTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
 AAAAA

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR
 VTRVAWLNRSTILYAGNDKWKCLDPRVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHFK
 TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGREPTVTWRHISPXAVGVFSEDEYL
 EIQGITREQSGDYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVQGKGLQCEASAV
 PSAEFQWYKDKRLRIELGKKGVKVENRPFSLKLIFFNVSEHDYGNYTCVASNKLGHTNASIML
 FPGAVAGVNSGNTSSRRAGCVMLPLLVLLHLLKLF

Signal peptide:

amino acids 1-28

FIGURE 53

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACCCAGAGCAAGGGCG
 GCAAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATCG
 AAGTTCAGGGGGCCCCGGCCTGCCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
 CCCCCGAGAGCGGAGAGGAAAGCACTGGGACAAAATATTGGGAGGCCCTTGGACATGGCC
 TGGGAGAGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA
 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCTGGCCACAGTGGTCTTTGGGAACTTCTGG
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCTGGAG
 GTCTGGGGACTCCGTGGGTCCACGGATACCCCGAAACTCAGCAGGCAGCTTTGGAATGAAT
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC
 TCAGGGAGCTGTGGCCCGCCTGGCTATGGTTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCTCTCTGGGGA
 TCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGCGGAGGAAATGGACATAAACC
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTGAGGCTTCA
 GAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTGGA
 GGCTCTGGAGACAATTATCGGGGGCAAGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGAGTCAATACTGTGAACCTTGAGACGTCTCCTGGGATGTTAACTTTGACACTTTCT
 GGAAGAAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGACCAGAGA
 AGCTCTCGCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT
 CCCTCCTTAAACACCAACCTCTCATCACTAATCTCAGCCCTTGCCCTTGAATAAACCTTA
 GCTGCCCCACAA
 AA

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
```

><MW: 42208, pI: 6.36, NX(S/T): 1

Signal peptide:

N-glycosylation site.

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT
 GGGGGTCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG
 AAGCTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGTATCCTGTCTCTGGACACCGG
 GTATCGCGCGCCGGTGACCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
 CGCAATCGA~~AC~~CCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACA**ACT**GAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
 GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
 TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
 AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
 CACCACCGAGGGGACCACCAGCCCTGGACAGCCATCGACCTCCAGGGTCCCTGCTGTGAGG
 GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTACCAGTGCTTACGCCACCACCCCT
 CCCCAGCACTACAGGTCTTGGCCCTGCTCCTCCAGTCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTATTCTTGCTGCTTCAGC
 CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNALHMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 57

GGAGCCGCCCTGGGTGTACGCGGCTCGGCTCCCGCGCAGCTCCGGCCGTGCGCAGCCTCG
 GCACCTGCAGGTCGGTGCCTCCGCGGCTGGCGCCCTGACTCCGTCCCGCCAGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
 GTGCCCTGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTTGCCCGCCAACCGTTGCAG
 GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC
 ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
 AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
 ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
 CAGCTGCTCCGTGAATGTGAAGACAAACAAGGCAAACTTAGGGGCCACAGCATCAAAACCT
 TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGTGTGCCCAT
 GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCAAAGGAGTAAGCCCGCTGTCCAATACCA
 GTGGGATCGGCAGCTTCCATCCTTCCAGACTTCTTTGCAACCAGATTAGATGTCAATCCGTG
 GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTCAAGGCCAC
 AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
 AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
 TCTTGTAACACCGCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
 ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
 TTCTCTGTCACTCCGACAGCCCTCCGGCCACCCCATGCCCCCTCCAGGCCCTGGTGCAT
 TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
 GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
 CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC
 CCCACCACTATTGGCTAAAGGATTGGGGTCTCTCCTTCTATAAGGGTACCTCTAGCAC
 AGAGGCCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
 TTTACTGTGGGAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
 AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
 CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
 CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGT
 ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
 TTATTAATAACTAACATGAAATATGTGTTGTTTCATTGCAAATTTAAATAAAGATACATAA
 TGTTTGTATGAAAA

7

Signal peptide:

Transmembrane domain:

N-glycosylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGTATTTTGCTGTTTATTTTTTTTTCTTTTCTTTTCCACACATTTGTATTTAT
 TTCCGTACTTCAGAAATGGGCGCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTCTCT
 GAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGGCTGCC
 CTAGTGTGTGCCGCTGCCACAGGAACTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
 TGGATTTCTGCAGAACTGCACAATGTACAGTCGGTGCACAGGCTACCTGTATGGCAACC
 AACTGGACGAATTTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTCAGGAAAAAC
 AATATTCAGACCATTTACAGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
 TCAAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTCTATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCG
 AGGGACACCTTCCAGCATCTCACCAGCTCAAGGAATTTCAATTGTACGTAATTCTCGTCTCC
 CACCTCCTCCGATCTCCAGGTACGCATCTGTACAGGCTCTATTTCGAGGACCAACAGAT
 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGAACAGGCTGGATATATCCA
 ACAACCACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTCTGAACAAGTCCGGG
 GGATGGCCGTGAGGAATTAATATGAATCTTTTGTCCTGTCCACCACGACCCCGCGCTG
 CCTCTCTTCAACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTAT
 TCCAAACCTTAGCAGAAGCTACACGCCCTCAAACCTCTACCACATCGAAACTTCCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCCACTATTCTGAAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAGTCAAGTCAAGTGGCTCTCTCTCTTACCCTGATGGCATA
 CAAACTCACATGGGTGAAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTTCAAGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCATCGATGCTTTTAACTACCGCGCGGTAGAAGACACATTGTTTCAGAGGC
 CACCACCATGCCCTCTATCTGAACAACGGCAGCAACAGCGTCCAGCCATGACGACGAGA
 CGTCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTCTGTCATATGCACAAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAATACAAACCGGGCGCGGGAAGATGATTATTGCGAGGCGAGGACCAAGA
 AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTAGATCGTCTCTTAAATTAACGAT
 CAACTCCTTAAAGGAGATTTAGACTGCAGCCCATTTACACCCCAATGGGGGCATTAATTA
 CACAGACTGCCATATCCCCAACACATGCGATCTGCAACAGCAGCGTGGCCAGACCTGGAGC
 ACTGCCATAGCTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAAATAGACTCTTTGAGAA
 CACACTCGTGTGTGCATATAAGACACGCAGATTACATTTGATATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTCTATTTCAAGTTAATTACAAACAGTTTGTAACTCTTGGCTTTTAAATCTT

FIGURE 60

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVLYGNQLDEFPMNLPKNVVRLHLQENNIQTI
 SRAALAQLLKLEELHLDNNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDSCSIKWVTEWLKYIPSSSLNVRGFMCGQPEQVRGMVAVRELNMNLLSCPTTTPGLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRRVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWKNRGRKKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
 DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
 522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAACTGTTATTACTGCTGCGTTT
 TATGTTGGGAATTCCTCTCCTATGGCCTTGCTCTGGAGCAACAGAAAACCTCTCAAAACAAAGA
 AAGTCAAGACGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
 TTTGTACCAGAGAAATGAATACGACTAGTCAACATCGGCCAGCTAAGATCTGATTTAGA
 CAATGGAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
 TTGATGAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
 TACATCTTTAAGAGCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
 GTTTGTCAATCAAGATTTCCGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
 AGGCCATTGTACAGAGATGTCTCCAGAAGAACATTAGTTATCCAGGTGACAGCAAGTGAT
 TGTACGATCCCTCAAGTGGTAATAATGCTCGTCTCTCTACAGCTTACTTCAAGGCCAGCC
 ATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTCAAATGGATAGAGAAC
 TGCAAGATGAGTATTGGGTAATCATTCAGCCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
 TCTGGAACAACAAGTGATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAA
 AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACACGATTGAAGAGGAT
 GATTGCGAAACATTTGACATTATTACTAATCATGAAACTCAAGAAGGATAGTTATATTTAA
 AAAGAAAGTGGATTTTGAGCACCAGAACCACATCGGTATTAGAGCAAAAGTTTAAACCATC
 ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCATTTCATTAAGATCCAG
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTCCATATATGTTATTGAAGTTTGTGA
 AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACCAATAGGAAT
 CTCCTATCAGGTATCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC
 ACTACAAGTAACCTCAGTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
 AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGGCAAGTTCTTAACATCA
 ATGATCATGCTCCTGAGTTCTCTCAATACATAGAGACTTATGTTTGTGAAAAATGCAAGCCTCT
 GGTCAAGTAATTCAGATCTCAGTGCAGTGGATAGAGATGAATCCATAGAAGACAGCATTTT
 TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTACAATCATAGATAATCAAG
 ATAACACAGCTGTCAATTTGACTAATAGAAGCTGGTTTAAACCTTCAAGAAGAACCTGTCTTC
 TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAGATACAAACACCTTAC
 CATCCATGCTCTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
 TGCTTTCCATGGATTCAAGACAGAAGTTATCATTGCTCATTGTGATTTGATGATCATATA
 TTTGGGTTTATTTTTTTGACTTTTGGGTTTAAAAACAACGGAGAAAAACAGATTCTATTTCTGA
 GAAAGTGAAGATTTAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAGAAG
 ATACAGAGGCCTTTGATATACGAGAGCTGAGGAGTAGTACCATAATGCCGGAACGCAAGACT
 CGGAAACCAACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
 CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
 CCCCCTCTTTGATTTCCCTCCAGACCTACGCTTTTGGGGGAACAGGCTCATTAGCTGGATCC
 CTGAGCTCCTTTAGAATCAGCAGTCTCTGATCAGGATGAAGATATGATTACCTTAATGAGTT
 GGGAGCTCGCTTTAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAATCAATATTAGG
 GCTTTTTACCATCAAAATTTTTAAAGTGCTAATGTGTATTGCAACCCAATGGTAGTCTTAA
 AGAGTTTTGTGCCCTGGCTCATGCGGGGAAAGCCCTAGTCTATGGAGTTTCTGATTTTCC
 CTGGAGTAATAATCTCCATGGTTATTTAAAGTACCTACATGCTGTCAATTGAAACAGAGATGG
 GGGAGAAATGTAACATCAGCTCACAGGCATCAATACAACAGATTGGAAGTAAATAATG
 TAGGAAGATATTAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
 CATATTTACTTAGGAAGAGTAAAAATACCAACGAGAAAAATTTAAAGGAGCAAAAATTTG
 CAAGTCAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAA
 ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT
 TTTAA

FIGURE 62

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKVKQPVRSRLRVKRGVWNQFFVPEEMNTTSHH
 IGQLRSDLNNGNNSFYQKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
 GRAVEPESEFVIKVSINDNEPKFLDEPYEAIVPMSPEGLVIQVTASDADDPSSGNNARL
 LYSLLQGQPYFVSVEPTTGIVIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLSD
 VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
 TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDPEPLFL
 PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFENINDNGTITTSNSLDREISA
 WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
 DESIEEHFHYFNLSVEDTNNSSTFIIDNQDNTAVILTNRGTGNLQEEPVFYISILIADNGIP
 SLTSTNTLTIHVDCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
 RRKQILFPEKSEDFRENI FQYDDEGGGEEDTEAFDIAELRSTIMRERKTRKTTSAEIRSLY
 RQSLQVGPDSAIFRKFILEKLEEA NTDP CAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQD
 ESYDYLNLGPFRKRLACMFGSAVQSNN

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCA**AATGGC**
 CGCCCTGCGAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCCCTGGCCACCAGCTGCCTCCTTC
 TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGAC
 AAGTCCAACCTTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
 CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
 TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAAGTGCTGTTC
 CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG
 CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
 AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGAGAGATCAAAGCAATTGGGAACTG
 GATTGCTGTTTATGTCTCTGAGAAATGCCTGCATT**TGAC**CCAGAGCAAAGCTGAAAAATGAA
 TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAC
 CAAAAGGAAGATGGGAAGCCAACCTCCATCATGATGGGTGGATTCCAATGAACCCCTGCGT
 TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
 TAGATATTTATTGATAACATTTCAATTGTAAGTGGTGTTCTATACACAGAAAAACAATTTATTT
 TTTAAATAATTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCTTTAGGGGAAAAACCC
 CTAATAGCTTCATGTTTCCATAATCAGTACTTTATATTATAAATGTATTATTATTATTA
 TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTATAGAAACATCATTG
 ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
 ATGTTTATTGACCTCAATAAACACTTGGATATCCC

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185
><subunit 1 of 1, 179 aa, 1 stop
><MW: 20011, pI: 8.10, NX(S/T): 3
MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:**Signal peptide:**

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 65

GCCCTAACCTTCCAGGGCTCAGCTCTTTGGAGCTGCCATTCTCCGGCTGCGAGAAAGGA
 CGCGCGCCCTGCGTCCGGCGAAGAAAAGAAGCAAACCTTGTCCGGAGGGTTTCGTATCAAC
 CTCCTTCCCGCAAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCTCTGCA
 GAGCCGACCGCCCTAGTGGATCTGGGGCAGGCAGCGGCGCTGGCTGTGGAATTAGATCTGT
 TTTGAACCCAGTGGAGCGCATCGTGGGGCTCGGAAGTCACCGTCCGCGGGCACC GGTTGG
 CGCTCCCGAGTGGAAACCGACAGTTTGCAGCCCTCGGCTGCAAGTGGCCCTCTCTCCCGCG
 GTTGTGTTCAGTGTCCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAAGAGAGCCCTCAGAGG
 TCCGAAGAGCGCTGCGCTCCTACTCGCGTTCGCTTCTTCTCTCTCGGTTCCCTACTGTGA
 AATCGCAGCGACATTTACAAAGGCCCTCGGGTCTACCGAGACCGATCCGCGAGCGTTTGGCC
 CGGTGCTGCTATTGTCATCGGGAGCCCCGAGCACCGGGCGAAATGCGCGAGGTTCCCGAAGGC
 CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTACGGACAGTTTCAGTTTCG
 CCGATGGGAAACCCGGAGACCAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCCTTCCCT
 CACACAGAGGAGGAGGTGGAAGTTGATTACACGCGTACAGCCACAGGTGGAAAGAACTT
 GGACTTCTCAAGGCGGTGACACGCAACCGAGCAAGCGTCCGCCAAGACTCTCCTGAGCCCA
 GAAGCTTCACAGCCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT
 ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATT
 ATGGGTGAACATACAGCAAAATGGAAAAAGATAAAGTGAAGTATGCGAATATTGTCCAATTA
 CTCATCGGCCAAGCTGCAAGAGTGAATCTGTCTTTCGATTTTCCATTTTATGGCCACTTCCTA
 CGTGAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGTCGTACATCGAATGCT
 AACAGCCACACAGTACATAGCACCTTTAATGGCAAAATTCGATCCCAGTGATCCAGAAAT
 CAACTGTGATATTTTATGATATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTC
 CAGGATAATTATAACCTGGGAAGCTTCACATTCAGGCAACCGTCTCATGGATGGACGAAT
 CATCTTTGGATACAAAGAAATTCCTGTCTTGGTACACAGATAAGTTCAACCAATCATCCAG
 TGAAGTCCGACTGTCCGATGCATTGTCTGTTGTCCACAGGATCCAAACAAATCCCAATGTT
 CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTACCAACAT
 TTCGGCTGTGGAGATGACCCCATTAACCATGCCTCCAGTTTAAACAGATGTGGCCCCGTGTG
 TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGA
 TTTGATCGTATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAAGTCAAAAGAGAAGAT
 GTGTGAGAAATACAGAACCGTGGAACTTCTTCTCGAACCACCAACCGTAGGAGCGACAA
 CACCCAGTTCCAGGTCCTAACTACCACAGAGAGCAGTGACTTCTCAATTTCCACCGAGC
 CTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA
 TGACAGTGCAGTGTGAGAAGAAAGGGGGAACCTCCACGCTGGCCTCATATTGGAATCCTCA
 TCCTGGTCTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCAACCA
 TCAGCAGCCAGCATCTTCTTTATTGAGAGAGCCCAAGCAGATGGCCTGCGATGAAGTTTGA
 AAGAGGCTCTGGACATCTGCCTATGCTGAAGTTGAACAGTTGGAGAGAAAGAGGCTTTA
 TTGTATCAGAGCAGTGCCTAAATTTCTAGGACAGAACAACACAGTACTGGTTTACAGGTGT
 TAAGACTAAAATTTTGCCTATACCTTTAAGACAACAACAACAACACACACAAACAGCTC
 TAAGCTGCTGTAGCCTGAAGAAGACAAGATTCTGGACAAGCTCAGGCCAGGAAACAAGGG
 TAAACAAAAAATAAACTTATACAAGATACCATTTTACACTGAACATAGAATTCCTAGTGG
 AATGTCTATCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA
 TAATGCTTTTGGCTTAGGTGTCAGGGTTGCAAGGATCAGAAAAAATAATATAATAAGC
 TTTAGTTCATGAGG

10002796.111501

FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTAQAFPHTEEEVEVDSSHAYS
 HRWKRNLDLFLKAVDTNRRASVGQDSPEPRSFDTLLDDGQDNNTQIEEDTDHNYIISRIYGPS
 DSASRDWLVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTG
 EVVHRMLTATQYIAPILMANFDPSVSRNSTVRYFDNGTALVVQWDHVLQDNYNLGSFTFQAT
 LLDMGRIIFGYKEIPVLVTQISSNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEHYRVELQ
 MSKITNISAVEMTPLPTCLQFNRCGPCVSSQIGFNCWSCKLQRCSSGFDRHRQDWVDSGCP
 EESKEKMCENTEPVETSSRTTTTVGATTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLK
 DNGASTDDSAAEKKGTLHAGLIIGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
 WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
 455-461

1002796.11501

FIGURE 67A

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGTCTGTTGCTCGAACCAGTGT
 GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCCTCCTGCCCTCCCGGCTGGACAGA
 GTGTGGACTTCCCTTGGGCGGCGGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTG
 CTTAGGTGTTATTGGGAAGATGGAGCTTCAAAGGGTGCCGTGCAGCCGGTCAAGTATTAT
 TTTTCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
 GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTTGTTCT
 GTTCAGACTCAACATACACCCAGAACAATGCAGGTGCATCTAATGTGCAAGTTCTCTCTAA
 GATATATGACATCTCAATGATATGACCGTCAATGAAGGAACCAACGTCACCTTACTTGT
 TGGCCACTGGGAACACAGAGCTTCCATTTCTGGCGACACATCTCCCATCAGCAAAACCA
 TTTGAAAATGGACAATATTGGACATTTATGGAATTAACAAGGGACAGGCTGGGGAATATGA
 ATGCAGTGCAGAAAATGATGTGTCATTTCCAGATGTGAGGAAAAGTAAAAGTTGTTGTCAACT
 TTGCTCCTACTATTTCAGGAATTAATCTGGCACCGTGACCCCGGACGTCAGTGGCCTGATA
 AGATGTGAAGGTGCAGGTGTGCCGCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT
 CTTCAATGGCCAAACAGGAATTTATTATCAAATTTTAGCACAAGATCCATTCTCATCTGTTA
 CCAACGTGACACAGGAGCACTTCGGCAATTATACCTGTGTGGCTGCCACAAGCTAGGCACA
 ACCAATCGCGAGCCTGCCCTTTAAACCTCCAAGTACAGCCAGTATGGAATTTACCGGGAGCGC
 TGATGTTCTTTTCTCCTGCTGGTACCTTTGTGTTGACACTGTCTCTTTTCCACGATATTCT
 ACCTGAAGAATGCCATTCTACAAATAATTCAAAGACCCATAAAAGGCTTTTAAAGGATTCTCT
 GAAAGTGTCTGATGGCTGGATCCAATCTGGTACAGTTTGTTAAAAGCAGCGTGGGATATAATC
 AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAAT
 TCTACTCTTTTTTGATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCCTTTTTTAAAG
 ACGTGAAGAGCTCGAAATTTACTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAACTAC
 AACTTTTCAAAGCAATTCAGTCATGGTCTGTAGGTGTCAGGCTGTAGTTTGCACAAAACGAA
 TATTGCAGTGAATATGTGATTTCTTAAAGGCTGCAATACAAGCATTCAGTTCCTCTGTTCAAT
 AAGATCCATCCACATTTACAAAGATGCATTTTTTTCTTTTGTGATAAAAGCAATATA
 TTGCCTTCAGATTATTTCTTCAAATATAACACATATCTAGATTTTTCTGCTCGCATGATAT
 TCAGGTTTCAGGAATGAGCCTTGAATATAACTGGCTGTGACAGCTCTGCTCTCTTTCTCTGT
 AAGTTCAGCATGGGTGTGCCTTCATACAATAATATTTTCTCTTTGCTCCCACTAATATAA
 AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCCAGAGTGATCAAGTTAAACCA
 TACATATCTCTAAGTACAAGAGGAGCTATTGGACTGTAAAAATCTCTCTCGCATGACAA
 TGGGTTTGTGAAATTTTGGCCCACTAATCACTAGTTCCTGTGATGAGAGCAATTTAATAAC
 AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGTCAAAAGTTAGATCCACGTTGGGA
 AATCATCTCCCTTTAAATGACAGCACAGTCCACTCAAAGGATGGCTGACAAATACAGCATCT
 TTTCTCTTCACTAGTCCAAGCCAAAAATTTAAGATGATTTGTGAGAAAGGGCACAAAGTCC
 TATCACCTAATATTACAAGAGTGTGGTAAGCGCTCATCATTAATTTATTTTGTGGCAGCTAA
 GTTAGATGACAGAGGAGCTGCTCCTGTGGACAGGAGCATTTGATATTTTCCATCTGAAA
 GTATCACTCAGTTGATGCTGGAATGCATGTTATATATTTTAAACATTCACAAAATATATA
 TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTTAAATAGCTAATTTCTCAATAA
 AATCTTTCTATATAGCCATTTTCAGTGCAACAAAGTAAAATCAAAAAGACCCTCTTTATTT
 TTCCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACAGTATGAGAATAT
 CTTAAGATTAAGATTAATCAAAATATTGTGAATGTTAAATTTTCTCATATAAAGAGCAAA
 AACTACATTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGTATGG
 TTTCACTCTTTTACTAAAGAAAGGCCATCACCTTGAAGGCCATTTTACAGGTTTGTATGAAGTT
 ACCAATTTTCAGTACACTAAATTTCTACAAATAGTCCCTTTTACAAGTTGTAACACAAAG
 ACCCTATAAAATAAATAGATACAAGAAATTTTGCAAGTGGTTATACATATTTGAGATATCTGAT
 TATGTTGCCCTAGCAGGAGTGGCTTAAAACTGTGATTTTTTTCTTCAAGTAAAACTTAGT
 CCCAAAGTACATCAAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG
 TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAAGTGAAT
 AAATATGATGACATATTTTGTATGATACATTAATAAGAGTTTGTAGAACAAATATGGCATTT
 TAACCTTATATTATTGCTTTTAAAGAAATATCTTTGTGGAATTTGTGAATAACTATATA
 AATATTATTTGTATTCAGCTTTAAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

FIGURE 67B

AGTGGTGTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAAGAACAGATC
 AAGAATGCATATTATTTCAGTGACCGCTTCTCTAGAGTTAAAAACCTCCTCTTTGTAAAGGTT
 TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAATAATTAGTTCAAAGTGTTGTCATG
 ATTCCAAATTTGTGGAGTCTGGTGTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
 CAGTAGCTATATGTATTGCTTTTATGTTAGAAGAGACTTCTCTGAGTGACATTTTAAATA
 GAGGAGGTATTCACTATGTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA
 CAGAGTGAATCATGAGTATTTATGAGTTCATATTGTCAAATAAGGCTACAGTATTTGCTT
 TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
 AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTCAGAATAG
 CAGTTTTATAAATGATTTATCTTTTAACTCTATAACAATTTGTGTTAGCTGTTTCATTTCAGG
 ANTATATTTTCTACAAGTTCCTACTTGTGGGACTCCTTTTGTGGCCCTATTTTTTTTTAAAG
 AAGGAAGAAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAAGAAAAAGATG
 AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
 AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGAAGGAAGAATCAGAGTATTAGG
 GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAACATGTTTTTCAA
 TGATCGCATTTGAAACATAAGTCCATTATATACCATTAAAGTTCCTATTATGCAGCAATTATAT
 AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGAGACACTAAAAGATTTGAG
 AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATACTTAACTGAAAAATTAATG
 CTTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGGAACTGAGAAAAATACCCAG
 GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
 ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
 TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
 ATAAAAATTTGTTTTTGAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
 TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
 GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTCCTGTCTTTTAGTAAAA
 CATCCATATTTCTAAACCTGATGTAAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC
 TCAGTTTATCAATTAAAAA

FIGURE 68

```
></usr/seqdb2/ss/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
><MW: 38719, pI: 6.12, NX(S/T): 6
MDMMLLVQGACCSNQWLAAVLLSLCLLPFSLPAGQSVDFPWAAVDMMVMVRKGDТАVLRСYЛ
EDGASKGAWLNRSSIIIFAGGDKWSVDPRVSISTLNKRDYSLQIQNVDTVDDGPTYCСVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYECSAENDVSFFDPVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGKTLFNGQGQGI I IQNFSRSLITVNTVTQEHFGNYTCVAANKLGTТNASL
PLNPSTAOYKGTGSADVLFSЦWYLVLTLSSTSI FYLKNAILQ
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.

amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327

Myelin P0 protein.

amino acids 94-123

FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACA
ATTTACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCAGTTGTTTTTG
TTCTCACGGCTTCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
TTAATTAAGGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGAC**ATGT**TATAGACACAAAA
CAGCTGGAGATTGGGCTTAAATATCCACCAAGCTCCAAAGAAGAGACCAAGTCCCCAAAA
CATTGATTTACAGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
GCCCACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC
CGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCAG
GCCAGTGCCGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC
ACCCCCCAGCAATCCGCGCGCCGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCT
TCTCCTCTGCAAA**TAG**

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175
><subunit 1 of 1, 155 aa, 1 stop
><MW: 17194, pI: 10.44, NX(S/T): 0
MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features of the protein:**Transmembrane domain:**

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

FIGURE 71

GTCTGTGCTTGGAGGAAGCCGCGGAACCCACGCTCCGTCC**ATG**GCGTGGAGCCTTGGGA
 GCTGGCTGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAAATGTC
 AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG
 GAACCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCGAAGATAATGCATGAATA
 CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
 AGGGCTGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCTGTGGATGA
 CACCATTATTGGACCCCTGGAATGCAAGTAGAAGTACTTGTGATTCTTTACATATGCGTT
 TCTTAGCCCCATAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCA
 TGGACTTATAATGTGCAATACTGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA
 GTATGACTTTGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAGTTCGAG
 GGTTCCTCTCTGATCGGAACAAAGCTGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAAC
 CATGACGAAACGGTCCCTCCTGGATGGTGGCCGTATCCTCATGGCCTCGGTCTTCATGGT
 CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAGACAAAGTACG
 CCTTCTCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
 AACACACTTCTGTTTTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAG
 TGTCAATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
 CCCCCTGGGCAGGGGCCCCAAGCT**TAG**GCTCTGAGAAGGAAACACACTCGGCTGGGCACA
 GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGATCAGGGCAGCAAAACAAGGGCCAAGA
 CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
 TTTAAAGGCTGTCTTGCAAAAATACTCCATTTGGGAACCTACTGCCCTATAAAGGCTTTCA
 TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTACGCCCTTTATATCACTAAAAATAA
 GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGCTCACGCCGTGAATACCAGCA
 CCTTAGAGGTGAGGCAGGCGGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATA
 TGGTGAAACCCAGTCTCTACTAAAAATACAAAATTAGCTAGGCATGATGGCGCATGCCTAT
 AATCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
 GGTTCAGTGAGCCGAGATAGCGGCACTGCATCCAGCCTGGGTGACAAAGTGAGACTCCAT
 CTCAAAAAATAAATAAATAAATTGTGAGAAACAGAAATACTTAAATGAGGAATAAGAATGG
 AGATGTTACATCTGGTAGATGTAACATTCTACAGATTATGGATGGACTGATCTGAAAATCG
 ACCTCAACTCAAGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGAATCTTTGCA
 GTACTTTGAATTTATTTTCTACCTATATATGTTTTATATGCTGCTGGTGCTCCATTAAAGT
 TTTACTCTGTGTTGC

10002795 - 111501
 10002795 - 111501

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551

><subunit 1 of 1, 325 aa, 1 stop

><MW: 37011, pI: 5.09, NX(S/T): 4

MAWSLGSWLGGCLLVSAIGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSQVNVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTT
YCVQVRGFLPDRNKAGEWSEPVEQTTTHDETVPSSWMAVILMASVFMVCLALLGCFSLWCV
YKTKYAFSPRNSLPQHLKEFLGPHHNTLLFFSPLSDENDVFDKLSVIAEDSESGKQNP
DSCSLGTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

FIGURE 73

CGAGCGCCAAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCCGCTCGCCGCCCGCCATGCGCCC
 GCGCAGCCCCGCTGCTCGCCGCGTTGACCGCGCTCCTCGCCGCCCGCGCTGCTGGCCGGAGAT
 GCCCCGCCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT
 TCTCCAGCAGCACTTTGGACCTCGGGTGACAGTTCGACGTGTACGAGAAGGGAACCGTGGGTG
 GCCGCTTGGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCTCCTTCCAC
 TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT
 GGTGGGCGAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC
 TGCTGAACCTCTTCCGCCCTCTGGTGGCAGTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG
 GTGGAGGAGGTCATGGAGAAATTCTAGGAGTCTATAAGTACCAGGCCACGGCTATGCGCTT
 CTCGGGTGTGGAGGAGCTGCTCTACTCAGTGGGGAGTCCACCTTTGTTAAACATGACCCAGC
 ACTCTGTGGCTGAGTCCTGCTGCAGGTGGGCGCTCAGCAGCGCTTATTGATGATGTCGTT
 TCTGCTGTCTCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCGCTTTGCGAGGAGCCAT
 GTCATAGCCGGGGCCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGTTTGT
 CCGGTTTGTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCCCTG
 CACAGCAGAGGGGAAAGCCCTGTACAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC
 TGACTCTATGACATCGTGGTCATCGCCACCCCTGCACCTGGACAACAGCAGCAACCT
 TAACCTTTGCGAGGCTTCCACCCGCCATTGATGACGTGCAGGGCTCTTCCAGCCACCGCTC
 GTCTCCTTGGTCCACGGCTACCTCAACTCGTCTACTTCCGTTTCCCAGACCTTAAGCTTTT
 CCCCTTTGCCAACATCCTTACCACAGATTTCCCAGCTTCTTCTGCACCTCTGGACAACATCT
 GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCGCTGTTTGGCGA
 GTCCAGTCCCCAAGCCCTCTTTCGGAGCCAGCTAAAGACCTGTTCCGTTCCTATTACTC
 AGTGCAAGACGCTGAGTGGCAGGCCCATCCCCCTCATGGCTCCCGCCCCACGCTCCCGAGGT
 TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGCGGCCAGCTCCGTGGAG
 GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGTGGCTTACAACCGCTGGTACCAGGACCT
 AGACAAGATTGATCAAAAAGATTGATGCACAAGGTCAAGACTGAACCTGTGAGGGCTCTAGG
 GAGAGCCTGGAACTTTTCATCCCCACTGAAGATGGATCATCCCACAGCAGCCAGGACTGA
 ATAAGCCATGCTCGCCACCAGGCTTCTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
 ACCTACTGTCTGCCTATATTAAAGGTCACACGCGCGCTGCTGCTTTTTTTTAAAGGGGAAA
 GTAAGAAAAGAGAAGGAATCCAAGCCAGTATATTTGTTTTATTATTTTTTTTAAAGAAGAA
 AAAAGTTTCACTCTTCAAGGTGCTTCAGACTTGTTTCTTAGCTAGAAACAGAGACTACG
 GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCTACTACCTACTC
 CCACAATGGACAATCAATTGAGGCACCTTACAAGAAAACATTTACAACAGATGGTTACAAAA
 TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGTCTGTTTACTGTGGACT
 TGATGGATTGAAGTACCTAGTTTCAAGTCTCCTAGTCACCATCTCCAAGCCTGTCAACATC
 ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAGGAAGAGATGTGTGCTGAATAGTC
 GTCACCATATCTCCAAGCTTCTTGCAACCCAGTGGGAAAAGAAACATGCGAGGCTGAGGAA
 GAGGGAAGCTCTTCTTGGCCACTAGAGGAATTAGCCATTCTCTCTTATGCAAAAGATTGA
 GGAATGCACAATATAAAGAAGAGAAGTCCCAAGATGGTAGAGAGCAGTCATATCTTACCC
 TAGATGTTTCATCCAGCAGAGAAGAAAGAAGGTGTTGGGGTAGGATTCTTCAGAGGTAGC
 CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTGCTTTTCTTTGCTTT
 TTCTACAAACCTTAAAAACACTTGTGTTTTAAAGAAAGTAAGAGCCCTTTTCATTCAAAA
 AAAAAAAAAAAAAAAAAAAAAA

10002795.11501

FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510

><subunit 1 of 1, 494 aa, 1 stop

><MW: 54646, pI: 7.27, NX(S/T): 6

MARAAPLLAALTALLAAAAAGGDAPPCKIAVVGAGIGGSAVAHFLQQHFGRVQIDVYEKGT
VGGRLATISVKNQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTQRFIDDVSAVLRASYGQSAAMPAFAGAMSLAGAQQSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSIVHGYLNSSYFGFPDPKLPFANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEAADVVRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPYIGSRPTL
PRFALHDQLFYLNLEWAASSVEVMAVAANKVALLAYNRWYQDLKIDQKDLMHKVKTEL

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435